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PATENT  
Attorney Docket No.: 17726A-000420US

Assistant Commissioner for Patents  
Washington, D.C. 20231

On

*February 13, 2007*

TOWNSEND and TOWNSEND and CREW LLP

By:

*[Signature]*

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re application of:

LEE *et al.*

Application No.: 10/028,726

Filed: December 21, 2001

For: PRODUCTS AND METHODS FOR  
CONTROLLING THE SUPPRESSION  
OF THE NEOPLASTIC PHENOTYPE

Examiner: Not yet assigned

Art Unit: 1633

COMMUNICATION UNDER

37 C.F.R. §§ 1.821-1.825

AND

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

In response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, 37 C.F.R. §§ 1.821-1.825, mailed December 13, 2002, Applicants submit that the computer-readable form in the instant application is identical with that filed in Application No. 08/472,760, filed November 27, 1996. In accordance with 37 C.F.R. § 1.821(e), please use the computer-readable form filed in Application No. 08/472,760 as the computer-readable form for the instant application. A paper copy of the last filed Sequence Listing from Application No. 08/472,760 is submitted herewith. The information in the paper copy of the Sequence Listing is identical to that which is in the computer readable form, as required under 37 C.F.R. § 1.821(f).

It is understood that the Patent and Trademark Office will make the necessary changes in application number and filing date for the computer-readable form that will be used for the instant application.

Please amend the specification in adherence with 37 C.F.R. §§ 1.821-1.825 as follows.

**In the Specification:**

Please replace paragraph [152] beginning at page 27, line 15, with the following:

[152] --The hypothetical protein predicted from the nucleotide sequence was expected to have MW about 106 kD. The immunoprecipitated protein has a MW about 110-114 kD. The complete RB protein amino acid sequence (SEQ ID NO:2) is illustrated in Table 1. This complete sequence obtained from the newly reconstructed clone which contains the most 5' end stretch missing in the original cDNA clone Science, 235:1394-1399 (1987).